SPEC of 7/27/04 in eDAW

AMENDMENTS TO THE SPECIFICATION

Please replace the title of the invention on the cover page and on page 1, line 1 with the following title:

ANTI-IDIOTYPE ANTIBODIES TO MN PROTEINS AND MN POLYPEPTIDES

Please replace the paragraph on page 3, lines 26-31 with the following amended paragraph:

The MN protein has also been identified with the G250 antigen. Uemura et al., "Expression of Tumor-Associated Antigen MN/G250 in Urologic Carcinoma: Potential Therapeutic Target, " ~~J. Urol., 154~~ **J. Urol., 157** (4 Suppl.): 377 (Abstract 1475; 1997) states: "Sequence analysis and database searching revealed that G250 antigen is identical to MN, a human tumor-associated antigen identified in cervical carcinoma (Pastorek et al., 1994)."

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Please replace the Table 1 on page ~~26~~ with the following amended Table 1:

TABLE 1
Exon-Intron Structure of the Human MN Gene

Exon	Size	Genomic Position**	SEQ ID NO	5'splice ~~acceptor~~ **donor**	SEQ ID NO
1	445	*3507-3951	28	AGAAG gtaagt	67
2	30	5126-5155	29	TGGAG gtgaga	68
3	171	5349-5519	30	CAGTC gtgagg	69
4	143	5651-5793	31	CCGAG gtgagc	70
5	93	5883-5975	32	TGGAG gtacca	71
6	67	7376-7442	33	GGAAG gtcagt	72
7	158	8777-8934	34	AGCAG gtgggc	73
8	145	9447-9591	35	GCCAG gtacag	74
9	27	9706-9732	36	TGCTG gtgagt	75

10	82	10350-~~70431~~ **10431**	37	CACAG gtatta	76
11	191	10562-10752	38	ATAAT end	

Intron	Size	Genomic Position **	SEQ ID NO	3'splice acceptor	SEQ ID NO
1	1174	3952-5125	39	atacag GGGAT	77
2	193	5156-5348	40	ccccag GCGAC	78
3	131	5520-5650	41	acgcag TGCAA	79
4	89	5794-5882	42	tttcag ATCCA	80
5	1400	5976-7375	43	ccccag GAGGG	81
6	1334	7443-8776	44	tcacag GCTCA	82
7	512	8935-9446	45	ccctag CTCCA	83
8	114	9592-9705	46	ctccag TCCAG	84
9	617	9733-10349	47	tcgcag GTGACA	85
10	130	10432-10561	48	acacag AAGGG	86

** positions are related to nt numbering in whole genomic sequence including the 5' flanking region [Figure 2A-F]

* number corresponds to transcription initiation site determined below by RNase protection assay

Please replace the paragraph on page 44, lines 13-18 with the following paragraph:

To identify the protein involved or the formation of a specific complex with the MN promoter in the PR4 region, relevant ds oligonucleotides covalently bound to magnetic beads will be used to purify the corresponding transcription factor. Alternatively the ONE Hybrid System® [Clontech (Palo Alto, CA (USA); **an in vivo yeast genetic assay for isolating genes encoding proteins that bind to a target, cis-actiging regulatory element or any other short DNA-binding sequence**] will be

used to search for and clone transcription factors involved in regulation of the analysed promoter region. A cDNA library from HeLa cells will be used for that investigation.

Please replace the paragraph on page 57, lines 9-17 with the following paragraph:

The conditioned media and the cell extracts were dot blotted onto nitrocellulose paper. The blot was blocked with 5% non-fat dried milk in PBS. Mab M75 were used to detect the MN 20-19 protein in the dot blots. A rabbit anti-mouse Ig-HRP was used to detect bound Mab M75. The blots were developed with TMB/H_2O_2 with a membrane enhancer [KPL; Gaithersburg, MD (USA)]. Two clones producing the strongest reaction on the dot blots were selected for expansion. One was used to produce MN 20-19 protein in High Five™ cells [Invitrogen Corp., San Diego, CA (USA); BTI-TN-5BI-4; derived from Trichoplusia ni egg cell homogenate]. MN 20-19 protein was purified from the conditioned media from the virus infected High Five™ cells.

Please replace the paragraph on page 58, lines 8-13 with the following paragraph:

Techniques of chemical peptide synthesis include using automatic peptide synthesizers employing commercially available protected amino acids, for example, Biosearch [San Rafael, CA (USA)] Models 9500 and 9600; Applied Biosystems, Inc. [Foster City, CA (USA)] Model 430; Milligen [a division of Millipore Corp.; Bedford, MA (USA)] Model 9050; and Du Pont's RAMP™ (Rapid Automated Multiple Peptide Synthesis) [Du Pont Compass, Wilmington, DE (USA)].

Please replace the paragraph on page 74, lines 5-12 with the following amended paragraph:

Epitope mapping was performed by the Novatope® system, a kit for which is commercially available from Novagen, Inc. [See, for analogous example, Li et al., Nature, 363: 85-88 (6 May 1993).] In brief, the MN cDNA was cut into overlapping short fragments of approximately 60 base pairs. The fragments were expressed in E. coli, and the E. coli colonies were transferred onto nitrocellulose paper, lysed and probed with the mab of interest. The MN cDNA of clones reactive with the mab of interest was sequenced, and the epitopes of the mabs were deduced from the overlapping polypeptides found to be reactive with each mab.

AMENDMENTS TO THE SEQUENCE LISTING

The information for SEQ ID NO: 76 in the Sequence Listing has been amended as follows:

<210> 76
<211> 11
<212> DNA
<213> HUMAN

<400> 76
~~atacaggggat~~ **cacaggtatt a** 11